

0300

#3



OIKE

RAW SEQUENCE LISTING
 PATENT APPLICATION: US/10/071,275

DATE: 02/27/2002
 TIME: 13:48:34

P.5

Input Set : A:\10448-139001.txt
 Output Set: N:\CRF3\02272002\J071275.raw

ENTERED

4 <110> APPLICANT: Meyers, Rachel E.
 6 <120> TITLE OF INVENTION: 80091, A NOVEL HUMAN UBIQUITIN
 7 CARBOXY-TERMINAL HYDROLASE FAMILY MEMBER AND USES THEREOF
 10 <130> FILE REFERENCE: 10448-139001
 C--> 12 <140> CURRENT APPLICATION NUMBER: US/10/071,275
 C--> 12 <141> CURRENT FILING DATE: 2002-02-07
 12 <150> PRIOR APPLICATION NUMBER: 60/267,054
 13 <151> PRIOR FILING DATE: 2001-02-07
 15 <160> NUMBER OF SEQ ID NOS: 7
 17 <170> SOFTWARE: FastSEQ for Windows Version 4.0
 19 <210> SEQ ID NO: 1
 20 <211> LENGTH: 3954
 21 <212> TYPE: DNA
 22 <213> ORGANISM: Homo sapiens
 24 <220> FEATURE:
 25 <221> NAME/KEY: CDS
 26 <222> LOCATION: (1)...(3951)
 28 <400> SEQUENCE: 1
 29 atg gtg gct gat gcc tgt aat ccc aac agt ttg gga gac tgg gga gga 48
 30 Met Val Ala Asp Ala Cys Asn Pro Asn Ser Leu Gly Asp Trp Gly Gly
 31 1 5 10 15
 33 aga tca ttt gag gcc agg agt ttg aga cca gcc tgg gct caa gca gtc 96
 34 Arg Ser Phe Glu Ala Arg Ser Leu Arg Pro Ala Trp Ala Gln Ala Val
 35 20 25 30
 37 ctg cct cag cct ccc aaa gtg ctg gga tta cag atg ggt cat ctt act 144
 38 Leu Pro Gln Pro Pro Lys Val Leu Gly Leu Gln Met Gly His Leu Thr
 39 35 40 45
 41 ctg gaa gac tat cag atc tgg agt gtg aaa aat gtt ctt gcc aat gag 192
 42 Leu Glu Asp Tyr Gln Ile Trp Ser Val Lys Asn Val Leu Ala Asn Glu
 43 50 55 60
 45 ttt ttg aac ctc ctt ttc cag gtg tgt cac ata gtt ctg ggg tta aga 240
 46 Phe Leu Asn Leu Leu Phe Gln Val Cys His Ile Val Leu Gly Leu Arg
 47 65 70 75 80
 49 cca gct act ccg gaa gaa gaa gga caa att att aga gga tgg tta gaa 288
 50 Pro Ala Thr Pro Glu Glu Glu Gly Gln Ile Ile Arg Gly Trp Leu Glu
 51 85 90 95
 53 cga gag agc agg tat ggt ctg caa gca gga cac aac tgg ttt atc atc 336
 54 Arg Glu Ser Arg Tyr Gly Leu Gln Ala Gly His Asn Trp Phe Ile Ile
 55 100 105 110
 57 tcc atg cag tgg tgg caa cag tgg aaa gaa tat gtc aaa tac gat gcc 384
 58 Ser Met Gln Trp Trp Gln Gln Trp Lys Glu Tyr Val Lys Tyr Asp Ala
 59 115 120 125
 61 aac cct gtg gta att gag cca tca tct gtt ttg aat gga gga aaa tac 432

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62 Asn Pro Val Val Ile Glu Pro Ser Ser Val Leu Asn Gly Gly Lys Tyr
63      130      135      140
65 tca ttt gga act gca gcc cat cct atg gag cag gtc gaa gat aga att      480
66 Ser Phe Gly Thr Ala Ala His Pro Met Glu Gln Val Glu Asp Arg Ile
67 145      150      155      160
69 gga agc agc ctc agt tac gtg aat act aca gaa gag aaa ttt tca gac      528
70 Gly Ser Ser Leu Ser Tyr Val Asn Thr Thr Glu Glu Lys Phe Ser Asp
71      165      170      175
73 aac att tct act gca tct gaa gcc tca gaa act gct ggc agc ggc ttt      576
74 Asn Ile Ser Thr Ala Ser Glu Ala Ser Glu Thr Ala Gly Ser Gly Phe
75      180      185      190
77 ctg tat tct gcc aca cca ggg gca gat gtt tgc ttt gct cga caa cat      624
78 Leu Tyr Ser Ala Thr Pro Gly Ala Asp Val Cys Phe Ala Arg Gln His
79      195      200      205
81 aac act tct gac aat aac aac cag tgt ttg ctg gga gcc aat ggg aat      672
82 Asn Thr Ser Asp Asn Asn Asn Gln Cys Leu Leu Gly Ala Asn Gly Asn
83      210      215      220
85 att ttg ttg cac ctt aac cct cag aaa cca ggg gct att gat aat cag      720
86 Ile Leu Leu His Leu Asn Pro Gln Lys Pro Gly Ala Ile Asp Asn Gln
87 225      230      235      240
89 cca tta gta act caa gaa cca gta aag gct aca tca tta aca cta gaa      768
90 Pro Leu Val Thr Gln Glu Pro Val Lys Ala Thr Ser Leu Thr Leu Glu
91      245      250      255
93 gga gga cga tta aaa cga act cca cag ctg att cat gga aga gac tat      816
94 Gly Gly Arg Leu Lys Arg Thr Pro Gln Leu Ile His Gly Arg Asp Tyr
95      260      265      270
97 gaa atg gtc cca gaa cct gtg tgg aga gca ctt tat cac tgg tat gga      864
98 Glu Met Val Pro Glu Pro Val Trp Arg Ala Leu Tyr His Trp Tyr Gly
99      275      280      285
101 gca aac ctg gcc tta cct aga cca gtt atc aag aac agc aag aca gac      912
102 Ala Asn Leu Ala Leu Pro Arg Pro Val Ile Lys Asn Ser Lys Thr Asp
103      290      295      300
105 atc cca gag ctg gaa tta ttt ccc cgc tat ctt ctc ttc ctg aga cag      960
106 Ile Pro Glu Leu Glu Leu Phe Pro Arg Tyr Leu Leu Phe Leu Arg Gln
107 305      310      315      320
109 cag cct gcc act cgg aca cag cag tct aac atc tgg gtg aat atg gga      1008
110 Gln Pro Ala Thr Arg Thr Gln Gln Ser Asn Ile Trp Val Asn Met Gly
111      325      330      335
113 aat gta cct tct ccg aat gca cct tta aag cgg gta tta gcc tat aca      1056
114 Asn Val Pro Ser Pro Asn Ala Pro Leu Lys Arg Val Leu Ala Tyr Thr
115      340      345      350
117 ggc tgt ttt agt cga atg cag acc atc aag gaa att cac gaa tat cta      1104
118 Gly Cys Phe Ser Arg Met Gln Thr Ile Lys Glu Ile His Glu Tyr Leu
119      355      360      365
121 tct caa aga ctg cgc att aaa gag gaa gat atg cgc ctg tgg cta tac      1152
122 Ser Gln Arg Leu Arg Ile Lys Glu Glu Asp Met Arg Leu Trp Leu Tyr
123      370      375      380
125 aac agt gag aac tac ctt act ctt ctg gat gat gag gat cat aaa ttg      1200
126 Asn Ser Glu Asn Tyr Leu Thr Leu Leu Asp Asp Glu Asp His Lys Leu

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127	385		390		395		400	
129	gaa	tat	ttg	aaa	atc	cag	gat	gaa
130	Glu	Tyr	Leu	Lys	Ile	Gln	Asp	Glu
131				405				410
133	aac	aaa	gat	atg	agt	tgg	cct	gag
134	Asn	Lys	Asp	Met	Ser	Trp	Pro	Glu
135				420				425
137	agt	aaa	ata	gat	aga	cac	aag	gtt
138	Ser	Lys	Ile	Asp	Arg	His	Lys	Val
139				435				440
141	cta	agc	aat	ctg	gga	aac	aca	tgc
142	Leu	Ser	Asn	Leu	Gly	Asn	Thr	Cys
143				450				455
145	gtt	agt	aac	aca	cag	cca	ctg	aca
146	Val	Ser	Asn	Thr	Gln	Pro	Leu	Thr
147	465							470
149	ctt	tat	gaa	ctc	aac	agg	aca	aat
150	Leu	Tyr	Glu	Leu	Asn	Arg	Thr	Asn
151								485
153	gct	aaa	tgc	tat	ggt	gat	tta	gtg
154	Ala	Lys	Cys	Tyr	Gly	Asp	Leu	Val
155				500				505
157	aag	aat	gtt	gcc	cca	tta	aag	ctt
158	Lys	Asn	Val	Ala	Pro	Leu	Lys	Leu
159				515				520
161	ccc	agg	ttt	aat	ggg	ttt	cag	caa
162	Pro	Arg	Phe	Asn	Gly	Phe	Gln	Gln
163				530				535
165	ttt	ctc	ttg	gat	ggt	ctt	cat	gaa
166	Phe	Leu	Leu	Asp	Gly	Leu	His	Glu
167	545							550
169	cca	tat	gtg	gaa	ctg	aag	gac	agt
170	Pro	Tyr	Val	Glu	Leu	Lys	Asp	Ser
171								565
173	gct	gca	gag	gcc	tgg	gac	aac	cat
174	Ala	Ala	Glu	Ala	Trp	Asp	Asn	His
175				580				585
177	gtg	gat	ttg	ttc	cat	ggg	cag	cta
178	Val	Asp	Leu	Phe	His	Gly	Gln	Leu
179				595				600
181	tgt	ggg	cat	ata	agt	gtc	cga	ttt
182	Cys	Gly	His	Ile	Ser	Val	Arg	Phe
183				610				615
185	cca	cta	cca	atg	gac	agt	tat	atg
186	Pro	Leu	Pro	Met	Asp	Ser	Tyr	Met
187	625							630
189	tta	gat	ggt	act	acc	cct	gta	cgg
190	Leu	Asp	Gly	Thr	Thr	Pro	Val	Arg
191				645				650

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193	gaa aag tac aca ggt tta aaa aaa cag ctg agt gat ctc tgt gga ctt	2016
194	Glu Lys Tyr Thr Gly Leu Lys Lys Gln Leu Ser Asp Leu Cys Gly Leu	
195	660 665 670	
197	aat tca gaa caa atc ctt cta gca gaa gta cat ggt tcc aac ata aag	2064
198	Asn Ser Glu Gln Ile Leu Leu Ala Glu Val His Gly Ser Asn Ile Lys	
199	675 680 685	
201	aac ttt cct cag gac aac caa aaa gta cga ctc tca gtg agt gga ttt	2112
202	Asn Phe Pro Gln Asp Asn Gln Lys Val Arg Leu Ser Val Ser Gly Phe	
203	690 695 700	
205	ttg tgt gca ttt gaa att cct gtc cct gtg tct cca att tca gct tct	2160
206	Leu Cys Ala Phe Glu Ile Pro Val Pro Val Ser Pro Ile Ser Ala Ser	
207	705 710 715 720	
209	agt cca aca cag aca gat ttc tcc tct tcg cca tct aca aat gaa atg	2208
210	Ser Pro Thr Gln Thr Asp Phe Ser Ser Ser Pro Ser Thr Asn Glu Met	
211	725 730 735	
213	ttc acc cta act acc aat ggg gac cta ccc cga cca ata ttc atc ccc	2256
214	Phe Thr Leu Thr Thr Asn Gly Asp Leu Pro Arg Pro Ile Phe Ile Pro	
215	740 745 750	
217	aat gga atg cca aac act gtt gtg cca tgt gga act gag aag aac ttc	2304
218	Asn Gly Met Pro Asn Thr Val Val Pro Cys Gly Thr Glu Lys Asn Phe	
219	755 760 765	
221	aca aat gga atg gtt aat ggt cac atg cca tct ctt cct gac agc ccc	2352
222	Thr Asn Gly Met Val Asn Gly His Met Pro Ser Leu Pro Asp Ser Pro	
223	770 775 780	
225	ttt aca ggt tac atc att gca gtc cac cga aaa atg atg agg aca gaa	2400
226	Phe Thr Gly Tyr Ile Ile Ala Val His Arg Lys Met Met Arg Thr Glu	
227	785 790 795 800	
229	ctg tat ttc ctg tca tct cag aag aat cgc ccc agc ctc ttt gga atg	2448
230	Leu Tyr Phe Leu Ser Ser Gln Lys Asn Arg Pro Ser Leu Phe Gly Met	
231	805 810 815	
233	cca ttg att gtt cca tgt act gtg cat acc cgg aag aaa gac cta tat	2496
234	Pro Leu Ile Val Pro Cys Thr Val His Thr Arg Lys Lys Asp Leu Tyr	
235	820 825 830	
237	gat gcg gtt tgg att caa gta tcc cgg tta gcg agc cca ctc cca cct	2544
238	Asp Ala Val Trp Ile Gln Val Ser Arg Leu Ala Ser Pro Leu Pro Pro	
239	835 840 845	
241	cag gaa gct agt aat cat gcc cag gat tgt gac gac agt atg ggc tat	2592
242	Gln Glu Ala Ser Asn His Ala Gln Asp Cys Asp Asp Ser Met Gly Tyr	
243	850 855 860	
245	caa tat cca ttc act cta cga gtt gtg cag aaa gat ggg aac tcc tgt	2640
246	Gln Tyr Pro Phe Thr Leu Arg Val Val Gln Lys Asp Gly Asn Ser Cys	
247	865 870 875 880	
249	gct tgg tgc cca tgg tat aga ttt tgc aga ggc tgt aaa att gat tgt	2688
250	Ala Trp Cys Pro Trp Tyr Arg Phe Cys Arg Gly Cys Lys Ile Asp Cys	
251	885 890 895	
253	ggg gaa gac aga gct ttc att gga aat gcc tat atc gct gtg gat tgg	2736
254	Gly Glu Asp Arg Ala Phe Ile Gly Asn Ala Tyr Ile Ala Val Asp Trp	
255	900 905 910	
257	gat ccc aca gcc ctt cac ctt cgc tat caa aca tcc cag gaa agg gtt	2784

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258	Asp	Pro	Thr	Ala	Leu	His	Leu	Arg	Tyr	Gln	Thr	Ser	Gln	Glu	Arg	Val	
259			915					920					925				
261	gta	gat	gag	cat	gag	agt	gtg	gag	cag	agt	cgg	cga	gcg	caa	gcc	gag	2832
262	Val	Asp	Glu	His	Glu	Ser	Val	Glu	Gln	Ser	Arg	Arg	Ala	Gln	Ala	Glu	
263			930					935					940				
265	ccc	atc	aac	ctg	gac	agc	tgt	ctc	cgt	gct	ttc	acc	agt	gag	gaa	gag	2880
266	Pro	Ile	Asn	Leu	Asp	Ser	Cys	Leu	Arg	Ala	Phe	Thr	Ser	Glu	Glu	Glu	
267	945					950					955					960	
269	cta	ggg	gaa	aat	gag	atg	tac	tac	tgt	tcc	aag	tgt	aag	acc	cac	tgc	2928
270	Leu	Gly	Glu	Asn	Glu	Met	Tyr	Tyr	Cys	Ser	Lys	Cys	Lys	Thr	His	Cys	
271				965						970					975		
273	tta	gca	aca	aag	aag	ctg	gat	ctc	tgg	agg	ctt	cca	ccc	atc	ctg	att	2976
274	Leu	Ala	Thr	Lys	Lys	Leu	Asp	Leu	Trp	Arg	Leu	Pro	Pro	Ile	Leu	Ile	
275				980					985					990			
277	att	cac	ctt	aag	cga	ttt	caa	ttt	gta	aat	ggt	cgg	tgg	ata	aaa	tca	3024
278	Ile	His	Leu	Lys	Arg	Phe	Gln	Phe	Val	Asn	Gly	Arg	Trp	Ile	Lys	Ser	
279			995					1000					1005				
281	cag	aaa	att	gtc	aaa	ttt	cct	cgg	gaa	agt	ttt	gat	cca	agt	gct	ttt	3072
282	Gln	Lys	Ile	Val	Lys	Phe	Pro	Arg	Glu	Ser	Phe	Asp	Pro	Ser	Ala	Phe	
283		1010					1015					1020					
285	ttg	gta	cca	aga	gac	ccg	gct	ctc	tgc	cag	cat	aaa	cca	ctc	aca	ccc	3120
286	Leu	Val	Pro	Arg	Asp	Pro	Ala	Leu	Cys	Gln	His	Lys	Pro	Leu	Thr	Pro	
287	1025					1030					1035				1040		
289	cag	ggg	gat	gag	ctc	tct	gag	ccc	agg	att	ctg	gca	agg	gag	gtg	aag	3168
290	Gln	Gly	Asp	Glu	Leu	Ser	Glu	Pro	Arg	Ile	Leu	Ala	Arg	Glu	Val	Lys	
291				1045					1050				1055				
293	aaa	gtg	gat	gcg	cag	agt	tcg	gct	ggg	gaa	gag	gac	gtg	ctc	ctg	agc	3216
294	Lys	Val	Asp	Ala	Gln	Ser	Ser	Ala	Gly	Glu	Glu	Asp	Val	Leu	Leu	Ser	
295				1060					1065				1070				
297	aaa	agc	cca	tcc	tca	ctc	agc	gct	aac	atc	atc	agc	agc	ccg	aaa	ggt	3264
298	Lys	Ser	Pro	Ser	Ser	Leu	Ser	Ala	Asn	Ile	Ile	Ser	Ser	Pro	Lys	Gly	
299			1075					1080					1085				
301	tct	cct	tct	tca	tca	aga	aaa	agt	gga	acc	agc	tgt	ccc	tcc	agc	aaa	3312
302	Ser	Pro	Ser	Ser	Ser	Arg	Lys	Ser	Gly	Thr	Ser	Cys	Pro	Ser	Ser	Lys	
303		1090					1095					1100					
305	aac	agc	agc	cct	aat	agc	agc	cca	cgg	act	ttg	ggg	agg	agc	aaa	ggg	3360
306	Asn	Ser	Ser	Pro	Asn	Ser	Ser	Pro	Arg	Thr	Leu	Gly	Arg	Ser	Lys	Gly	
307	1105					1110					1115			1120			
309	agg	ctc	cgg	ctg	ccc	cag	att	ggc	agc	aaa	aat	aaa	ctg	tca	agt	agt	3408
310	Arg	Leu	Arg	Leu	Pro	Gln	Ile	Gly	Ser	Lys	Asn	Lys	Leu	Ser	Ser	Ser	
311				1125					1130				1135				
313	aaa	gag	aac	ttg	gat	gcc	agc	aaa	gaa	aat	ggg	gct	ggg	cag	ata	tgt	3456
314	Lys	Glu	Asn	Leu	Asp	Ala	Ser	Lys	Glu	Asn	Gly	Ala	Gly	Gln	Ile	Cys	
315				1140					1145				1150				
317	gag	ctg	gct	gac	gcc	ttg	agt	cga	ggg	cat	gtg	ctg	ggg	ggc	agc	caa	3504
318	Glu	Leu	Ala	Asp	Ala	Leu	Ser	Arg	Gly	His	Val	Leu	Gly	Gly	Ser	Gln	
319			1155					1160					1165				
321	cca	gag	ttg	gtc	act	cct	cag	gac	cat	gag	gta	gct	ttg	gcc	aat	gga	3552
322	Pro	Glu	Leu	Val	Thr	Pro	Gln	Asp	His	Glu	Val	Ala	Leu	Ala	Asn	Gly	

Use of n and / or Xaa has been detected in the Sequence Listing. Review the Sequence Listing to ensure a corresponding explanation is present in the <220> to <223> fields of each sequence using n or Xaa.

VERIFICATION SUMMARY

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L:12 M:270 C: Current Application Number differs, Replaced Current Application No

L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:590 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5